

# SEQUENCE LISTING

<110> Liaw, Chen W.  
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Leonard, James N.  
Ortuno, Daniel  
Lin, I-Lin

<120> Endogenous And Non-Endogenous, Constitutively Activated G Protein-Coupled Receptors

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<170> PatentIn version 3.1

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Trp Val Ala Gly Phe Arg Met Thr Arg Thr Val Asn Thr Ile Cys Tyr  
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Arg Met Val Ser Val Ala Met Arg Glu Lys Trp Pro Phe Gly Ser Phe  
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Leu Cys Lys Leu Val His Val Met Ile Asp Ile Asn Leu Phe Val Ser  
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Val Tyr Leu Ile Thr Ile Ile Ala Leu Asp Arg Cys Ile Cys Val Leu  
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Asn Ser Leu Val Leu Val Ile Ser Ile Phe Tyr His Lys Leu Gln Ser  
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Thr Val Arg Trp His Phe Gly Asp His Phe Cys Arg Leu Ser Ala Thr  
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Phe Val Gly Phe Ser Leu Cys Trp Leu Pro His Ser Val Tyr Ser Leu  
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Thr Ser Thr Cys Val Leu Trp Phe Ser Tyr Leu Lys Ser Val Phe Asn  
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Gln Pro Lys Arg Ala Thr Val Glu Gly Phe Asp Ala Tyr Phe Thr Ser  
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Val Met Phe Asn Lys Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe  
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Gln Tyr Gln Thr Thr Asn Thr Ser Asn Pro Gly Tyr Arg Leu Ile Gly  
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Lys Gly Val Arg Glu Ile Pro Ala Ser Val Cys Thr Leu Pro Cys Lys

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Ala Val Val Thr Ala Ala Thr Met Ser Ser Arg Leu Ser His Lys Pro  
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Ala Ala Gly Arg Gly Ala Glu Ala Ser Ala Ala Gly Pro Pro Gly Pro  
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Pro Thr Arg Pro Pro Gly Pro Trp Arg Trp Lys Gly Ala Arg Gly Gln  
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Ile Ser Gly Arg Ser Gln Glu Gln Ser Val Lys Thr Val Pro Gly Ala  
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His His Lys Pro Leu Ser Lys Thr Ala Asn Gly Leu Ala Gly His Glu



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Asn Tyr Tyr Met Arg Ser Ile Ser Asn Ser Leu Leu Ala Asn Leu Ala  
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Phe Trp Asp Phe Leu Ile Ile Phe Phe Cys Leu Pro Leu Val Ile Phe  
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His Glu Leu Thr Lys Lys Trp Leu Leu Glu Asp Phe Ser Cys Lys Ile  
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<212> PRT
<213> Unknown

<220>
<223> Novel Sequence

<400> 12

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Met Ser Pro Glu Cys Ala Arg Ala Ala Gly Asp Ala Pro Leu Arg Ser
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Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys
20          25          30

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Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val

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45

Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser  
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Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu  
275 280 285

Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe  
290 295 300

Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu  
305 310 315 320

Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys  
325 330 335

Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys  
340 345 350

Arg Asn Asp Leu Ser Ile Ile Ser Gly  
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<400> 14

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Leu Asn Leu Thr Asp Glu Ala Leu Arg Leu Lys Tyr Leu Gly Pro Gln  
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Gln Thr Glu Leu Phe Met Pro Ile Cys Ala Thr Tyr Leu Leu Ile Phe  
35 40 45

Val Val Gly Ala Val Gly Asn Gly Leu Thr Cys Leu Val Ile Leu Arg  
50 55 60

His Lys Ala Met Arg Thr Pro Thr Asn Tyr Tyr Leu Phe Ser Leu Ala  
65 70 75 80

Val Ser Asp Leu Leu Val Leu Leu Val Gly Leu Pro Leu Glu Leu Tyr  
85 90 95

Glu Met Trp His Asn Tyr Pro Phe Leu Leu Gly Val Gly Gly Cys Tyr  
100 105 110

Phe Arg Thr Leu Leu Phe Glu Met Val Cys Leu Ala Ser Val Leu Asn  
115 120 125

Val Thr Ala Leu Ser Val Glu Arg Tyr Val Ala Val Val His Pro Leu  
130 135 140

Gln Ala Arg Ser Met Val Thr Arg Ala His Val Arg Arg Val Leu Gly  
145 150 155 160

Ala Val Trp Gly Leu Ala Met Leu Cys Ser Leu Pro Asn Thr Ser Leu  
165 170 175

His Gly Ile Arg Gln Leu His Val Pro Cys Arg Gly Pro Val Pro Asp  
180 185 190

Ser Ala Val Cys Met Leu Val Arg Pro Arg Ala Leu Tyr Asn Met Val  
195 200 205

Val Gln Thr Thr Ala Leu Leu Phe Phe Cys Leu Pro Met Ala Ile Met  
210 215 220

Ser Val Leu Tyr Leu Leu Ile Gly Leu Arg Leu Arg Arg Glu Arg Leu  
225 230 235 240

Leu Leu Met Gln Glu Ala Lys Gly Arg Gly Ser Ala Ala Ala Arg Ser  
245 250 255

Arg Tyr Thr Cys Arg Leu Gln Gln His Asp Arg Gly Arg Arg Gln Val  
260 265 270

Thr Lys Met Leu Phe Val Leu Val Val Phe Gly Ile Cys Trp Ala  
275 280 285

Pro Phe His Ala Asp Arg Val Met Trp Ser Val Val Ser Gln Trp Thr  
290 295 300

Asp Gly Leu His Leu Ala Phe Gln His Val His Val Ile Ser Gly Ile  
305 310 315 320

Phe Phe Tyr Leu Gly Ser Ala Ala Asn Pro Val Leu Tyr Ser Leu Met  
325 330 335

Ser Ser Arg Phe Arg Glu Thr Phe Gln Glu Ala Leu Cys Leu Gly Ala  
340 345 350

Cys Cys His Arg Leu Arg Pro Arg His Ser Ser His Ser Leu Ser Arg

355

360

365

Met Thr Thr Gly Ser Thr Leu Cys Asp Val Gly Ser Leu Gly Ser Trp  
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Asp Pro Ser

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 aacctggcgg tggccgacct ctgcctgctg tgcaccttgc ccttcgtgct gcaactccctg 240  
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 tacatgagca tcagcctggt caccggccat gccgtggacc gctatgtggc cgtgcggcac 360  
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<210> 16  
 <211> 309  
 <212> PRT



<213> Homo sapiens

<400> 16

Met Asn Gly Thr Tyr Asn Thr Cys Gly Ser Ser Asp Leu Thr Trp Pro  
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Pro Ala Ile Lys Leu Gly Phe Tyr Ala Tyr Leu Gly Val Leu Leu Val  
20 25 30

Leu Gly Leu Leu Leu Asn Ser Leu Ala Leu Trp Val Phe Cys Cys Arg  
35 40 45

Met Gln Gln Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val  
50 55 60

Ala Asp Leu Cys Leu Leu Cys Thr Leu Pro Phe Val Leu His Ser Leu  
65 70 75 80

Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu Ser Gln Gly Ile Tyr  
85 90 95

Leu Thr Asn Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val  
100 105 110

Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Gly Leu Arg  
115 120 125

Ser Pro Arg Gln Ala Ala Ala Val Cys Ala Val Leu Trp Val Leu Val  
130 135 140

Ile Gly Ser Leu Val Ala Arg Trp Leu Leu Gly Ile Gln Glu Gly Gly  
145 150 155 160

Phe Cys Phe Arg Ser Thr Arg His Asn Phe Asn Ser Met Arg Phe Pro  
165 170 175

Leu Leu Gly Phe Tyr Leu Pro Leu Ala Val Val Val Phe Cys Ser Leu  
180 185 190

Lys Val Val Thr Ala Leu Ala Gln Arg Pro Pro Thr Asp Val Gly Gln  
195 200 205

Ala Glu Ala Thr Arg Lys Ala Ala Arg Met Val Trp Ala Asn Leu Leu

210

215

220

Val Phe Val Val Cys Phe Leu Pro Leu His Val Gly Leu Thr Val Arg  
225 230 235 240

Leu Ala Val Gly Trp Asn Ala Cys Ala Leu Leu Glu Thr Ile Arg Arg  
245 250 255

Ala Leu Tyr Ile Thr Ser Lys Leu Ser Asp Ala Asn Cys Cys Leu Asp  
260 265 270

Ala Ile Cys Tyr Tyr Tyr Met Ala Lys Glu Phe Gln Glu Ala Ser Ala  
275 280 285

Leu Ala Val Ala Pro Arg Ala Lys Ala His Lys Ser Gln Asp Ser Leu  
290 295 300

Cys Val Thr Leu Ala  
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<210> 17  
<211> 1446  
<212> DNA  
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cagagccgat ccaagagggg caccgaggat gaggaggcca agggcggtgca gcagtatgtg 180  
cctgaggagt gggcggagta cccccggccc attcaccctg ctggcctgca gccaaccaag 240  
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gaactgaggg gcaatctgac aggggcacca gggcagaggc tacagatcca gaaccccctg 360  
tatccggtga ccgagagctc ctacagtgcc tatgccatca tgcttctggc gctggtggtg 420  
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ctgaagagcg cctggaactc catccttgcc agcctggccc tctgggattt tctggctctc 540  
ttttctgtcc tccctattgt catcttcaac gagatcacca agcagaggct actgggtgac 600  
gtttcttgtc gtgcctgtgc ctccatggag gtctctctc tgggagtcac gactttcagc 660  
ctctgtgccc tgggcattga ccgcttcac gtggccacca gcacctgcc caagggtgagg 720

cccatcgagc ggtgccaatc cactctggcc aagttggctg tcacttgggt gggctccatg 780  
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 cccatcctct tcacagtcac ctgccagctg gtgacatggc gggcgagag cctccagg 1020  
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 aaccagtctt ccacctttct caaggcgccc atcaccaccag tgctgtctct ttgcatctgc 1260  
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 <212> FRT  
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<400> 18

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Val Gly Leu Ser Arg Val Ser Gly Gly Ala Pro Leu His Leu Gly Arg  
 20 25 30

His Arg Ala Glu Thr Gln Glu Gln Gln Ser Arg Ser Lys Arg Gly Thr  
 35 40 45

Glu Asp Glu Glu Ala Lys Gly Val Gln Gln Tyr Val Pro Glu Glu Trp  
 50 55 60

Ala Glu Tyr Pro Arg Pro Ile His Pro Ala Gly Leu Gln Pro Thr Lys  
 65 70 75 80

Pro Leu Val Ala Thr Ser Pro Asn Pro Asp Lys Asp Gly Gly Thr Pro  
 85 90 95

Asp Ser Gly Gln Glu Leu Arg Gly Asn Leu Thr Gly Ala Pro Gly Gln  
100 105 110

Arg Leu Gln Ile Gln Asn Pro Leu Tyr Pro Val Thr Glu Ser Ser Tyr  
115 120 125

Ser Ala Tyr Ala Ile Met Leu Leu Ala Leu Val Val Phe Ala Val Gly  
130 135 140

Ile Val Gly Asn Leu Ser Val Met Cys Ile Val Trp His Ser Tyr Tyr  
145 150 155 160

Leu Lys Ser Ala Trp Asn Ser Ile Leu Ala Ser Leu Ala Leu Trp Asp  
165 170 175

Phe Leu Val Leu Phe Phe Cys Leu Pro Ile Val Ile Phe Asn Glu Ile  
180 185 190

Thr Lys Gln Arg Leu Leu Gly Asp Val Ser Cys Arg Ala Val Pro Phe  
195 200 205

Met Glu Val Ser Ser Leu Gly Val Thr Thr Phe Ser Leu Cys Ala Leu  
210 215 220

Gly Ile Asp Arg Phe His Val Ala Thr Ser Thr Leu Pro Lys Val Arg  
225 230 235 240

Pro Ile Glu Arg Cys Gln Ser Ile Leu Ala Lys Leu Ala Val Ile Trp  
245 250 255

Val Gly Ser Met Thr Leu Ala Val Pro Glu Leu Leu Leu Trp Gln Leu  
260 265 270

Ala Gln Glu Pro Ala Pro Thr Met Gly Thr Leu Asp Ser Cys Ile Met  
275 280 285

Lys Pro Ser Ala Ser Leu Pro Glu Ser Leu Tyr Ser Leu Val Met Thr  
290 295 300

Tyr Gln Asn Ala Arg Met Trp Trp Tyr Phe Gly Cys Tyr Phe Cys Leu  
305 310 315 320

Pro Ile Leu Phe Thr Val Thr Cys Gln Leu Val Thr Trp Arg Val Arg  
 325 330 335

Gly Pro Pro Gly Arg Lys Ser Glu Cys Arg Ala Ser Lys His Glu Gln  
 340 345 350

Cys Glu Ser Gln Leu Asn Ser Thr Val Val Gly Leu Thr Val Val Tyr  
 355 360 365

Ala Phe Cys Thr Leu Pro Glu Asn Val Cys Asn Ile Val Val Ala Tyr  
 370 375 380

Leu Ser Thr Glu Leu Thr Arg Gln Thr Leu Asp Leu Leu Gly Leu Ile  
 385 390 395 400

Asn Gln Phe Ser Thr Phe Phe Lys Gly Ala Ile Thr Pro Val Leu Leu  
 405 410 415

Leu Cys Ile Cys Arg Pro Leu Gly Gln Ala Phe Leu Asp Cys Cys Cys  
 420 425 430

Cys Cys Cys Cys Glu Glu Cys Gly Gly Ala Ser Glu Ala Ser Ala Ala  
 435 440 445

Asn Gly Ser Asp Asn Lys Leu Lys Thr Glu Val Ser Ser Ser Ile Tyr  
 450 455 460

Phe His Lys Pro Arg Glu Ser Pro Pro Leu Leu Pro Leu Gly Thr Pro  
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29

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 <211> 33  
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 <400> 26  
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 <211> 33  
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 <400> 27  
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 <210> 28  
 <211> 30  
 <212> DNA  
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 <400> 28  
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 <212> DNA  
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<400> 29  
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37

<210> 30  
<211> 39  
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<220>  
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<400> 30  
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39

<210> 31  
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<220>  
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<400> 31  
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39

<210> 32  
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<400> 32  
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35

<210> 33  
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<223> Novel Sequence

<400> 33  
gcgaattccg gctccctgtg ctgccccagg

30

<210> 34  
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<400> 34
gcggatcccg gagccccga gacctggccc 30

<210> 35
<211> 31
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<220>
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<400> 35
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<210> 36
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<220>
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<210> 37
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<220>
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<400> 37
tccagccgtc ccaaactgt cttcgtgc 29

<210> 38
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<400> 38
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<210> 39

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<220>  
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<400> 45  
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<212> DNA  
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<220>  
<223> Novel Sequence

<400> 46  
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34

<210> 47  
<211> 35  
<212> DNA  
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<220>  
<223> Novel Sequence

<400> 47  
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35

<210> 48  
<211> 35  
<212> DNA  
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<220>  
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<400> 53  
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<210> 54  
<211> 33  
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<400> 54  
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<210> 55  
<211> 29  
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<400> 55  
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<210> 56  
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<400> 56  
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<210> 57  
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<220>  
<223> Novel Sequence

<400> 57  
gagagccagc tcaagagcac cgtggtg 27

<210> 58

<211> 31  
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 <400> 58  
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 <210> 59  
 <211> 31  
 <212> DNA  
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 <220>  
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 <400> 59  
 agtggcactc cccctcggct gtgattcctg t 31  
  
 <210> 60  
 <211> 30  
 <212> DNA  
 <213> Unknown  
  
 <220>  
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 <400> 60  
 gccaccgcga aggcataaacg catggctctgg 30  
  
 <210> 61  
 <211> 31  
 <212> DNA  
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 <400> 61  
 ctctctcggt cctcctatcg ttgtcagaag t 31  
  
 <210> 62  
 <211> 1062  
 <212> DNA  
 <213> Unknown  
  
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 <223> Novel Sequence  
  
 <400> 62  
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ggccacacgg ttctgtggat ctctcattg ctagtccacg gagtcacctt tgtcttcggg 120  
 gtccctggga atgggcttgt gatctgggtg gctggattcc ggatgacacg cacagtcaac 180  
 accatctgtt acctgaacct ggccctagct gacttctctt tcagtgccat cctaccattc 240  
 cgaatggctc cagtcgcat gagagaaaaa tggccttttg gctcattcct atgtaagtta 300  
 gtctcatgta tgatagacat caacctgtt gtcagtgtct acctgatcac catcattgct 360  
 ctggaccgct gtatttgtgt cctgcatcca gcctgggccc agaaccatcg caccatgagt 420  
 ctggccaaga ggggatgac gggactctgg attttcacca tagtccttac ctacacaaat 480  
 ttcatcttct ggactacaat aagtactacg aatggggaca catactgtat ttcaacttt 540  
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 tatgggatca tcgctgcaa aattcacaga aaccacatga ttaaatacag cgtcccaaaa 720  
 cgtgtcttct cgctgtgtgt ggcctcttct ttcattctgt ggttccttta tgaactaatt 780  
 ggcattctaa tggcagctcg gctcaaagag atgttggtta atggcaata caaatcatt 840  
 ctgtctccta ttaacccaac aagctccttg gcctttttta acagctgcct caaccaatt 900  
 ctctacgtct ttatgggtcg taacttcaa gaaagactga ttgcctcttt gccactagt 960  
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<210> 63  
 <211> 353  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Novel Sequence  
 <400> 63

Met Glu Thr Asn Phe Ser Ile Pro Leu Asn Glu Thr Glu Glu Val Leu  
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Pro Glu Pro Ala Gly His Thr Val Leu Trp Ile Phe Ser Leu Leu Val  
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His Gly Val Thr Phe Val Phe Gly Val Leu Gly Asn Gly Leu Val Ile  
 35 40 45

Trp Val Ala Gly Phe Arg Met Thr Arg Thr Val Asn Thr Ile Cys Tyr  
50 55 60

Leu Asn Leu Ala Leu Ala Asp Phe Ser Phe Ser Ala Ile Leu Pro Phe  
65 70 75 80

Arg Met Val Ser Val Ala Met Arg Glu Lys Trp Pro Phe Gly Ser Phe  
85 90 95

Leu Cys Lys Leu Val His Val Met Ile Asp Ile Asn Leu Phe Val Ser  
100 105 110

Val Tyr Leu Ile Thr Ile Ile Ala Leu Asp Arg Cys Ile Cys Val Leu  
115 120 125

His Pro Ala Trp Ala Gln Asn His Arg Thr Met Ser Leu Ala Lys Arg  
130 135 140

Val Met Thr Gly Leu Trp Ile Phe Thr Ile Val Leu Thr Leu Pro Asn  
145 150 155 160

Phe Ile Phe Trp Thr Thr Ile Ser Thr Thr Asn Gly Asp Thr Tyr Cys  
165 170 175

Ile Phe Asn Phe Ala Phe Trp Gly Asp Thr Ala Val Glu Arg Leu Asn  
180 185 190

Val Phe Ile Thr Met Ala Lys Val Phe Leu Ile Leu His Phe Ile Ile  
195 200 205

Gly Phe Ser Val Pro Met Ser Ile Ile Thr Val Cys Tyr Gly Ile Ile  
210 215 220

Ala Ala Lys Ile His Arg Asn His Met Ile Lys Ser Ser Arg Pro Lys  
225 230 235 240

Arg Val Phe Ala Ala Val Val Ala Ser Phe Phe Ile Cys Trp Phe Pro  
245 250 255

Tyr Glu Leu Ile Gly Ile Leu Met Ala Val Trp Leu Lys Glu Met Leu  
260 265 270



Leu Asn Gly Lys Tyr Lys Ile Ile Leu Val Leu Ile Asn Pro Thr Ser  
275 280 285

Ser Leu Ala Phe Phe Asn Ser Cys Leu Asn Pro Ile Leu Tyr Val Phe  
290 295 300

Met Gly Arg Asn Phe Gln Glu Arg Leu Ile Arg Ser Leu Pro Thr Ser  
305 310 315 320

Leu Glu Arg Ala Leu Thr Glu Val Pro Asp Ser Ala Gln Thr Ser Asn  
325 330 335

Thr Asp Thr Thr Ser Ala Ser Pro Pro Glu Glu Thr Glu Leu Gln Ala  
340 345 350

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<210> 64  
<211> 1029  
<212> DNA  
<213> Unknown

<220>  
<223> Novel Sequence

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gtgtttgtct gtggtctggt ggggaactct ctggtgctgg tcatatccat ctctaccat 180  
aagttgcaga gcctgacgga tgtgttcctg gtgaacctac cctcggtga cctggtgttt 240  
gtctgcactc tgccttctg gccctatgca gccatccatg aatgggtgtt tggccaggtc 300  
atgtgcaaaa gcctactggg catctacact attaacttct acacgtccat gctcatcctc 360  
acctgcacga ctgtggatcg ttctattgta gtggttaagg ccaccaaggc ctacaaccag 420  
caagccaaga ggaatgacctg gggcaaggtc accagcttgc tcatctgggt gatatccctg 480  
ctggtttcct tgcctcaaat tatctatggc aatgtcttta atctcgacaa gctcatatgt 540  
ggttacatcg acgagggaat ttocactgtg gttcttgcca ccagatgac actgggggttc 600  
ttcttgccac tgctcaccat gattgtctgc tattcagtca taatcaaaac actgcttcat 660  
gctggaggct tccagaagca cagatcaaaa aagatcatct tctgtgtgat ggctgtgttc 720

ctgctgaccc agatgccctt caacctcatg aagttcatcc gcagcacaca ctgggaatac 780  
 tatgccatga ccagctttca ctacaccatc atgggtgacag aggccatgcg atacctgagg 840  
 gcttgccatta accctgtgct ctatgccctt gtcagcctga agtttcgaaa gaacttctgg 900  
 aaacttgtga aggacattgg ttgcctccct taccttgggg tctcacatca atggaaatct 960  
 tctgaggaca attccaagac tttttctgcc tcccacaatg tggaggccac cagcatgttc 1020  
 cagttatag 1029

<210> 65  
 <211> 342  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Novel Sequence

<400> 65

Met Ala Glu His Asp Tyr His Glu Asp Tyr Gly Phe Ser Ser Phe Asn  
 1 5 10 15

Asp Ser Ser Gln Glu Glu His Gln Ala Phe Leu Gln Phe Ser Lys Val  
 20 25 30

Phe Leu Pro Cys Met Tyr Leu Val Val Phe Val Cys Gly Leu Val Gly  
 35 40 45

Asn Ser Leu Val Leu Val Ile Ser Ile Phe Tyr His Lys Leu Gln Ser  
 50 55 60

Leu Thr Asp Val Phe Leu Val Asn Leu Pro Leu Ala Asp Leu Val Phe  
 65 70 75 80

Val Cys Thr Leu Pro Phe Trp Ala Tyr Ala Gly Ile His Glu Trp Val  
 85 90 95

Phe Gly Gln Val Met Cys Lys Ser Leu Leu Gly Ile Tyr Thr Ile Asn  
 100 105 110

Phe Tyr Thr Ser Met Leu Ile Leu Thr Cys Ile Thr Val Asp Arg Phe  
 115 120 125

Ile Val Val Val Lys Ala Thr Lys Ala Tyr Asn Gln Gln Ala Lys Arg  
 130 135 140

Met Thr Trp Gly Lys Val Thr Ser Leu Leu Ile Trp Val Ile Ser Leu  
145 150 155 160

Leu Val Ser Leu Pro Gln Ile Ile Tyr Gly Asn Val Phe Asn Leu Asp  
165 170 175

Lys Leu Ile Cys Gly Tyr His Asp Glu Ala Ile Ser Thr Val Val Leu  
180 185 190

Ala Thr Gln Met Thr Leu Gly Phe Phe Leu Pro Leu Leu Thr Met Ile  
195 200 205

Val Cys Tyr Ser Val Ile Ile Lys Thr Leu Leu His Ala Gly Gly Phe  
210 215 220

Gln Lys His Arg Ser Lys Lys Ile Ile Phe Leu Val Met Ala Val Phe  
225 230 235 240

Leu Leu Thr Gln Met Pro Phe Asn Leu Met Lys Phe Ile Arg Ser Thr  
245 250 255

His Trp Glu Tyr Tyr Ala Met Thr Ser Phe His Tyr Thr Ile Met Val  
260 265 270

Thr Glu Ala Ile Ala Tyr Leu Arg Ala Cys Leu Asn Pro Val Leu Tyr  
275 280 285

Ala Phe Val Ser Leu Lys Phe Arg Lys Asn Phe Trp Lys Leu Val Lys  
290 295 300

Asp Ile Gly Cys Leu Pro Tyr Leu Gly Val Ser His Gln Trp Lys Ser  
305 310 315 320

Ser Glu Asp Asn Ser Lys Thr Phe Ser Ala Ser His Asn Val Glu Ala  
325 330 335

Thr Ser Met Phe Gln Leu  
340

<210> 66  
<211> 2748  
<212> DNA

<213> Unknown

<220>

<223> Novel Sequence

<400> 66

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cactcaatcc ggatcgagg ggacgtcacc ctcggggggc tgttcccgt gcacgccaa	180
ggtcccacgc gagtgcctg cggcgacatc aagagggaaa acgggatcca caggctggaa	240
gcatgtctct acgccttga ccagatcaac agtgatccca acctactgcc caacgtgacg	300
ctgggcgcgc ggatcctgga cacttgttcc agggacactt acgcgtctga acagtgcgtt	360
actttctgcc aggcgtcat ccagaaggac acctccgacg tgcgtgcac caacgcgcaa	420
ccgcgcgttt tctgtcaagg ggagaaagta gttggagtga ttggggcttc ggggagttcg	480
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gtgtctaccc tcgcctcgga aggaagttaa ggagagaaag gtgtggagtc cttcacgcag	720
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agggccgtcg tgatttttgc caacgatgag gatataaagc agatccttgc agcagccaaa	900
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aaccactgc accagcatga agatatcgca gaaggggcca tcaccattca gcccaagcga	1020
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tcaaaaaaag aagacacaga tcgcaaatgc acaggacagg agagaattgg aaaagattcc	1200
aactatgacg agggggtaa agtccagttc gtgattgagc cagtctatgc tatggctcac	1260
gcccttcacc acatgaacaa ggatctctgt gctgactacc ggggtgtctg ccagagatg	1320
gagcaagctg gaggcaagaa gttgctgaag tatatacgca atgttaattt caatggtagt	1380
gctggcactc cagtgatgtt taacaagaac ggggatgcac ctgggcgtta tgacatcttt	1440
cagtaccaga ccacaaacac cagcaaccog ggttaccgtc tgatcgggca gtggacagac	1500
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<210> 67  
<211> 915  
<212> PRT  
<213> Unknown

<220>  
<223> Novel Sequence

<400> 67

Met Val Gln Leu Arg Lys Leu Leu Arg Val Leu Thr Leu Met Lys Phe  
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Pro Cys Cys Val Leu Glu Val Leu Leu Cys Ala Leu Ala Ala Ala Ala

Arg Gly Gln Glu Met Tyr Ala Pro His Ser Ile Arg Ile Glu Gly Asp  
35 40 45

Val Thr Leu Gly Gly Leu Phe Pro Val His Ala Lys Gly Pro Ser Gly  
50 55 60

Val Pro Cys Gly Asp Ile Lys Arg Glu Asn Gly Ile His Arg Leu Glu  
65 70 75 80

Ala Met Leu Tyr Ala Leu Asp Gln Ile Asn Ser Asp Pro Asn Leu Leu  
85 90 95

Pro Asn Val Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp  
100 105 110

Thr Tyr Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Gln  
115 120 125

Lys Asp Thr Ser Asp Val Arg Cys Thr Asn Gly Glu Pro Pro Val Phe  
130 135 140

Val Lys Pro Glu Lys Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser  
145 150 155 160

Val Ser Ile Met Val Ala Asn Ile Leu Arg Leu Phe Gln Ile Pro Gln  
165 170 175

Ile Ser Tyr Ala Ser Thr Ala Pro Glu Leu Ser Asp Asp Arg Arg Tyr  
180 185 190

Asp Phe Phe Ser Arg Val Val Pro Pro Asp Ser Phe Gln Ala Gln Ala  
195 200 205

Met Val Asp Ile Val Lys Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu  
210 215 220

Ala Ser Glu Gly Ser Tyr Gly Glu Lys Gly Val Glu Ser Phe Thr Gln  
225 230 235 240

Ile Ser Lys Glu Ala Gly Gly Leu Cys Ile Ala Gln Ser Val Arg Ile  
245 250 255

Pro Gln Glu Arg Lys Asp Arg Thr Ile Asp Phe Asp Arg Ile Ile Lys  
260 265 270

Gln Leu Leu Asp Thr Pro Asn Ser Arg Ala Val Val Ile Phe Ala Asn  
275 280 285

Asp Glu Asp Ile Lys Gln Ile Leu Ala Ala Ala Lys Arg Ala Asp Gln  
290 295 300

Val Gly His Phe Leu Trp Val Gly Ser Asp Ser Trp Gly Ser Lys Ile  
305 310 315 320

Asn Pro Leu His Gln His Glu Asp Ile Ala Glu Gly Ala Ile Thr Ile  
325 330 335

Gln Pro Lys Arg Ala Thr Val Glu Gly Phe Asp Ala Tyr Phe Thr Ser  
340 345 350

Arg Thr Leu Glu Asn Asn Arg Arg Asn Val Trp Phe Ala Glu Tyr Trp  
355 360 365

Glu Glu Asn Phe Asn Cys Lys Leu Thr Ile Ser Gly Ser Lys Lys Glu  
370 375 380

Asp Thr Asp Arg Lys Cys Thr Gly Gln Glu Arg Ile Gly Lys Asp Ser  
385 390 395 400

Asn Tyr Glu Gln Glu Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr  
405 410 415

Ala Met Ala His Ala Leu His His Met Asn Lys Asp Leu Cys Ala Asp  
420 425 430

Tyr Arg Gly Val Cys Pro Glu Met Glu Gln Ala Gly Gly Lys Lys Leu  
435 440 445

Leu Lys Tyr Ile Arg Asn Val Asn Phe Asn Gly Ser Ala Gly Thr Pro  
450 455 460

Val Met Phe Asn Lys Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe  
465 470 475 480

Gln	Tyr	Gln	Thr	Thr	Asn	Thr	Ser	Asn	Pro	Gly	Tyr	Arg	Leu	Ile	Gly
			485						490					495	
Gln	Trp	Thr	Asp	Glu	Leu	Gln	Leu	Asn	Ile	Glu	Asp	Met	Gln	Trp	Gly
			500					505					510		
Lys	Gly	Val	Arg	Glu	Ile	Pro	Ala	Ser	Val	Cys	Thr	Leu	Pro	Cys	Lys
		515					520					525			
Pro	Gly	Gln	Arg	Lys	Lys	Thr	Gln	Lys	Gly	Thr	Pro	Cys	Cys	Trp	Thr
	530					535					540				
Cys	Glu	Pro	Cys	Asp	Gly	Tyr	Gln	Tyr	Gln	Phe	Asp	Glu	Met	Thr	Cys
545					550					555					560
Gln	His	Cys	Pro	Tyr	Asp	Gln	Arg	Pro	Asn	Glu	Asn	Arg	Thr	Gly	Cys
				565					570					575	
Gln	Asp	Ile	Pro	Ile	Ile	Lys	Leu	Glu	Trp	His	Ser	Pro	Ser	Ala	Val
			580					585					590		
Ile	Pro	Val	Phe	Leu	Ala	Met	Leu	Gly	Ile	Ile	Ala	Thr	Ile	Phe	Val
		595					600					605			
Met	Ala	Thr	Phe	Ile	Arg	Tyr	Asn	Asp	Thr	Pro	Ile	Val	Arg	Ala	Ser
	610					615					620				
Gly	Arg	Glu	Leu	Ser	Tyr	Val	Leu	Leu	Thr	Gly	Ile	Phe	Leu	Cys	Tyr
625					630					635					640
Ile	Ile	Thr	Phe	Leu	Met	Ile	Ala	Lys	Pro	Asp	Val	Ala	Val	Cys	Ser
			645						650					655	
Phe	Arg	Arg	Val	Phe	Leu	Gly	Leu	Gly	Met	Cys	Ile	Ser	Tyr	Ala	Ala
			660					665					670		
Leu	Leu	Thr	Lys	Thr	Asn	Arg	Ile	Tyr	Arg	Ile	Phe	Glu	Gln	Gly	Lys
		675					680					685			
Lys	Ser	Val	Thr	Ala	Pro	Arg	Leu	Ile	Ser	Pro	Thr	Ser	Gln	Leu	Ala
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<211> 2748  
<212> DNA  
<213> Unknown

<220>  
<223> Novel Sequence

<400> 68  
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cactcaatcc ggatcgaggg ggacgtcacc ctcggggggc tgttccccgt gacgcccaag 180  
ggtccacgcg gagtgcctct cgccgacatc aagagggaaa acgggatcca caggctggaa 240  
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ccgcgggttt tctgcaagcc ggagaaagta gttggagtga ttggggcttc ggggagttcg 480  
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cccgatctct tcaaagccca ggccatggta gacattgtaa aggccctagg ctggaattat 660  
gtgtctaccc tcgcatcgga aggaagttat ggagagaaag gtgtggagtc ctacacgcag 720  
atttccaaaaggcagggtg actctgcatt gcccagtcgg tgagaatccc ccaggaacgc 780  
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aatgtatggt ttgccgaata ctgggaggaa aacttcaact gcaagttgac gattagtggg 1140  
tcaaaaaaag aagacacaga tcgcaaatgc acaggacagg agagaattgg aaaagattcc 1200  
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cagtaccaga ccacaaacac cagcaacccg ggttaccgtc tgatcgggca gtggacagac 1500

gaacttcagc tcaatataga agacatgcag tggggtaaaag gagtccgaga gatacccgcc 1560  
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 ttcttgggct tgggtatgtg catcagttat gcagccctct tgacgaaaac aaatcggaatt 2040  
 tatcgcatat ttgagcaggg caagaaatca gtaacagctc ccagactcat aagcccaaca 2100  
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 ggatatagca ttcttctcat ggtcacatgt actgtgtatg ccacacagac tcgggggtgta 2340  
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 tggcttgctt tcatccaat tttttttggc accgctcaat cagcggaaaa gctctacata 2460  
 caaactacca cgcttacaat ctccatgaac ctaagtgcac cagtggcgct ggggatgcta 2520  
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<210> 69  
 <211> 915  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Novel Sequence

<400> 69

Met Val Gln Leu Arg Lys Leu Leu Arg Val Leu Thr Leu Met Lys Phe  
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Pro Cys Cys Val Leu Glu Val Leu Leu Cys Ala Leu Ala Ala Ala Ala  
20 25 30 .

Arg Gly Gln Glu Met Tyr Ala Pro His Ser Ile Arg Ile Glu Gly Asp  
35 40 45

Val Thr Leu Gly Gly Leu Phe Pro Val His Ala Lys Gly Pro Ser Gly  
50 55 60

Val Pro Cys Gly Asp Ile Lys Arg Glu Asn Gly Ile His Arg Leu Glu  
65 70 75 80

Ala Met Leu Tyr Ala Leu Asp Gln Ile Asn Ser Asp Pro Asn Leu Leu  
85 90 95

Pro Asn Val Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp  
100 105 110

Thr Tyr Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Gln  
115 120 125

Lys Asp Thr Ser Asp Val Arg Cys Thr Asn Gly Glu Pro Pro Val Phe  
130 135 140

Val Lys Pro Glu Lys Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser  
145 150 155 160

Val Ser Ile Met Val Ala Asn Ile Leu Arg Leu Phe Gln Ile Pro Gln  
165 170 175

Ile Ser Tyr Ala Ser Thr Ala Pro Glu Leu Ser Asp Asp Arg Arg Tyr  
180 185 190

Asp Phe Phe Ser Arg Val Val Pro Pro Asp Ser Phe Gln Ala Gln Ala  
195 200 205

Met Val Asp Ile Val Lys Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu  
210 215 220

Ala Ser Glu Gly Ser Tyr Gly Glu Lys Gly Val Glu Ser Phe Thr Gln  
225 230 235 240

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89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100

Ile Ser Lys Glu Ala Gly Gly Leu Cys Ile Ala Gln Ser Val Arg Ile  
245 250 255

Pro Gln Glu Arg Lys Asp Arg Thr Ile Asp Phe Asp Arg Ile Ile Lys  
260 265 270

Gln Leu Leu Asp Thr Pro Asn Ser Arg Ala Val Val Ile Phe Ala Asn  
275 280 285

Asp Glu Asp Ile Lys Gln Ile Leu Ala Ala Ala Lys Arg Ala Asp Gln  
290 295 300

Val Gly His Phe Leu Trp Val Gly Ser Asp Ser Trp Gly Ser Lys Ile  
305 310 315 320

Asn Pro Leu His Gln His Glu Asp Ile Ala Glu Gly Ala Ile Thr Ile  
325 330 335

Gln Pro Lys Arg Ala Thr Val Glu Gly Phe Asp Ala Tyr Phe Thr Ser  
340 345 350

Arg Thr Leu Glu Asn Asn Arg Arg Asn Val Trp Phe Ala Glu Tyr Trp  
355 360 365

Glu Glu Asn Phe Asn Cys Lys Leu Thr Ile Ser Gly Ser Lys Lys Glu  
370 375 380

Asp Thr Asp Arg Lys Cys Thr Gly Gln Glu Arg Ile Gly Lys Asp Ser  
385 390 395 400

Asn Tyr Glu Gln Glu Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr  
405 410 415

Ala Met Ala His Ala Leu His His Met Asn Lys Asp Leu Cys Ala Asp  
420 425 430

Tyr Arg Gly Val Cys Pro Glu Met Glu Gln Ala Gly Gly Lys Lys Leu  
435 440 445

Leu Lys Tyr Ile Arg Asn Val Asn Phe Asn Gly Ser Ala Gly Thr Pro  
450 455 460

Val Met Phe Asn Lys Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe

[illegible]



<210> 70  
 <211> 2748  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Novel Sequence

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 ctggagggtgc tctctgtgcgc gctggcggcg gcggcgcgcg gccaggagat gtacgccccg 120  
 cactcaatcc ggatcgaggg ggacgtcacc ctcggggggc tgttccccgt gcacgccaag 180  
 ggtccaccgc gagtgcctct cggcgacatc aagagggaaa acgggatcca caggctggaa 240  
 gcgatgctct acgccctgga ccagatcaac agtgatccca acctactgcc caacgtgacg 300  
 ctgggcgcgc ggatcctgga cacttgttcc agggacaact acgcgctcga acagtcgctt 360  
 actttctgctc aggcgctcat ccagaaggac acctccgacg tgcgctgcac caacggcgaa 420  
 ccgcccgttt tcgtcaagcc ggagaaagta gttggagtga ttggggcttc ggggagttcg 480  
 gtctccatca tggtagccaa catcctgagg ctcttccaga tccccagat tagttatgca 540  
 tcaacggcac ccgagctaag tgatgaccgc cgctatgaet tcttctctcg cgtggtgcca 600  
 cccgattcct tccaagccca ggccatggtg gacattgtaa aggcctagg ctggaattat 660  
 gtgtctaccc tcgcatcgga aggaagttat ggagagaaa gtgtggagtc cttcacgcag 720  
 atttccaaa aggcagggtg actctgcatt gcccagtcgc tgagaatccc ccaggaaacgc 780  
 aaagacagga ccattgactt tgatagaatt atcaaacagc tcctggacac ccccaactcc 840  
 agggccgctg tgatttttgc caacgatgag gatataaagc agatccctgc agcagccaaa 900  
 agagctgacc aagttggcca ttttctttgg gtgggatcag acagctgggg atccaaaata 960  
 aaccactgc accagcatga agatatacga gaaggggcca tcaccattca gcccaagcga 1020  
 gccacggttg aagggtttga tgccacttt acgtcccga cacttgaaaa caacagaaga 1080  
 aatgtatggt ttgccgaata ctgggaggaa aacttcaact gcaagttgac gattagtggg 1140  
 tcaaaaaaa aagacacaga tcgcaaatgc acaggacagg agagaattgg aaaagattcc 1200  
 aactatgagc aggggggtaa agtccagttc gtgattgacg cagtctatgc tatggctcac 1260  
 gcccttcacc acatgaacaa ggatctctgt gctgactacc ggggtgtctg ccagagatg 1320  
 gagcaagctg gaggcaagaa gttgctgaag tatatacgca atgttaattt caatggtagt 1380  
 gctggcactc cagtgatgtt taacaagaac ggggatgcac ctgggcgtta tgacatcttt 1440





1	5	10	15
Pro Cys Cys Val Leu Glu Val Leu Leu Cys Ala Leu Ala Ala Ala	20	25	30
Arg Gly Gln Glu Met Tyr Ala Pro His Ser Ile Arg Ile Glu Gly Asp	35	40	45
Val Thr Leu Gly Gly Leu Phe Pro Val His Ala Lys Gly Pro Ser Gly	50	55	60
Val Pro Cys Gly Asp Ile Lys Arg Glu Asn Gly Ile His Arg Leu Glu	65	70	75
Ala Met Leu Tyr Ala Leu Asp Gln Ile Asn Ser Asp Pro Asn Leu Leu	85	90	95
Pro Asn Val Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp	100	105	110
Thr Tyr Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Gln	115	120	125
Lys Asp Thr Ser Asp Val Arg Cys Thr Asn Gly Glu Pro Pro Val Phe	130	135	140
Val Lys Pro Glu Lys Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser	145	150	155
Val Ser Ile Met Val Ala Asn Ile Leu Arg Leu Phe Gln Ile Pro Gln	165	170	175
Ile Ser Tyr Ala Ser Thr Ala Pro Glu Leu Ser Asp Asp Arg Arg Tyr	180	185	190
Asp Phe Phe Ser Arg Val Val Pro Asp Ser Phe Gln Ala Gln Ala	195	200	205
Met Val Asp Ile Val Lys Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu	210	215	220
Ala Ser Glu Gly Ser Tyr Gly Glu Lys Gly Val Glu Ser Phe Thr Gln	225	230	235
			240

Ile Ser Lys Glu Ala Gly Gly Leu Cys Ile Ala Gln Ser Val Arg Ile  
245 250 255

Pro Gln Glu Arg Lys Asp Arg Thr Ile Asp Phe Asp Arg Ile Ile Lys  
260 265 270

Gln Leu Leu Asp Thr Pro Asn Ser Arg Ala Val Val Ile Phe Ala Asn  
275 280 285

Asp Glu Asp Ile Lys Gln Ile Leu Ala Ala Ala Lys Arg Ala Asp Gln  
290 295 300

Val Gly His Phe Leu Trp Val Gly Ser Asp Ser Trp Gly Ser Lys Ile  
305 310 315 320

Asn Pro Leu His Gln His Glu Asp Ile Ala Glu Gly Ala Ile Thr Ile  
325 330 335

Gln Pro Lys Arg Ala Thr Val Glu Gly Phe Asp Ala Tyr Phe Thr Ser  
340 345 350

Arg Thr Leu Glu Asn Asn Arg Arg Asn Val Trp Phe Ala Glu Tyr Trp  
355 360 365

Glu Glu Asn Phe Asn Cys Lys Leu Thr Ile Ser Gly Ser Lys Lys Glu  
370 375 380

Asp Thr Asp Arg Lys Cys Thr Gly Gln Glu Arg Ile Gly Lys Asp Ser  
385 390 395 400

Asn Tyr Glu Gln Glu Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr  
405 410 415

Ala Met Ala His Ala Leu His His Met Asn Lys Asp Leu Cys Ala Asp  
420 425 430

Tyr Arg Gly Val Cys Pro Glu Met Glu Gln Ala Gly Gly Lys Lys Leu  
435 440 445

Leu Lys Tyr Ile Arg Asn Val Asn Phe Asn Gly Ser Ala Gly Thr Pro  
450 455 460

Val Met Phe Asn Lys Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe  
465 470 475 480

Gln Tyr Gln Thr Thr Asn Thr Ser Asn Pro Gly Tyr Arg Leu Ile Gly  
485 490 495

Gln Trp Thr Asp Glu Leu Gln Leu Asn Ile Glu Asp Met Gln Trp Gly  
500 505 510

Lys Gly Val Arg Glu Ile Pro Ala Ser Val Cys Thr Leu Pro Cys Lys  
515 520 525

Pro Gly Gln Arg Lys Lys Thr Gln Lys Gly Thr Pro Cys Cys Trp Thr  
530 535 540

Cys Glu Pro Cys Asp Gly Tyr Gln Tyr Gln Phe Asp Glu Met Thr Cys  
545 550 555 560

Gln His Cys Pro Tyr Asp Gln Arg Pro Asn Glu Asn Arg Thr Gly Cys  
565 570 575

Gln Asp Ile Pro Ile Ile Lys Leu Glu Trp His Ser Pro Trp Ala Val  
580 585 590

Ile Pro Val Phe Leu Ala Met Leu Gly Ile Ile Ala Thr Ile Phe Val  
595 600 605

Met Ala Thr Phe Ile Arg Tyr Asn Asp Thr Pro Ile Val Arg Ala Ser  
610 615 620

Gly Arg Glu Leu Ser Tyr Val Leu Leu Thr Gly Ile Phe Leu Cys Tyr  
625 630 635 640

Ile Ile Thr Phe Leu Met Ile Ala Lys Pro Asp Val Ala Val Cys Ser  
645 650 655

Phe Arg Arg Val Phe Leu Gly Leu Gly Met Cys Ile Ser Tyr Ala Ala  
660 665 670

Leu Leu Thr Lys Thr Asn Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys  
675 680 685

Lys Ser Val Thr Ala Pro Arg Leu Ile Ser Pro Thr Ser Gln Leu Ala  
690 695 700

Ile Thr Ser Ser Leu Ile Ser Val Gln Leu Leu Gly Val Phe Ile Trp  
705 710 715 720

Phe Gly Val Asp Pro Pro Asn Ile Ile Ile Asp Tyr Asp Glu His Lys  
725 730 735

Thr Met Asn Pro Glu Gln Ala Arg Gly Val Leu Lys Cys Asp Ile Thr  
740 745 750

Asp Leu Gln Ile Ile Cys Ser Leu Gly Tyr Ser Ile Leu Leu Met Val  
755 760 765

Thr Cys Cys Val Tyr Ala Ile Lys Thr Arg Gly Val Pro Glu Asn Phe  
770 775 780

Asn Glu Ala Lys Pro Ile Gly Phe Thr Met Tyr Thr Thr Cys Ile Val  
785 790 795 800

Trp Leu Ala Phe Ile Pro Ile Phe Phe Gly Thr Ala Gln Ser Ala Glu  
805 810 815

Lys Leu Tyr Ile Gln Thr Thr Thr Leu Thr Ile Ser Met Asn Leu Ser  
820 825 830

Ala Ser Val Ala Leu Gly Met Leu Tyr Met Pro Lys Val Tyr Ile Ile  
835 840 845

Ile Phe His Pro Glu Leu Asn Val Gln Lys Arg Lys Arg Ser Phe Lys  
850 855 860

Ala Val Val Thr Ala Ala Thr Met Ser Ser Arg Leu Ser His Lys Pro  
865 870 875 880

Ser Asp Arg Pro Asn Gly Glu Ala Lys Thr Glu Leu Cys Glu Asn Val  
885 890 895

Asp Pro Asn Ser Pro Ala Ala Lys Lys Lys Tyr Val Ser Tyr Asn Asn  
900 905 910

Leu Val Ile

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 <211> 2748  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Novel Sequence

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 cactcaatcc ggatcgaggg ggacgtcacc ctcggggggc tgttccccgt gcacgccaag 180  
 ggtcccacgc gagtgccctg cgccgacatc aagagggaaa acgggatcca caggctggaa 240  
 gcgatgctct acgccctgga ccagatcaac agtgatccca acctactgcc caacgtgacg 300  
 ctggcgcgcg ggatcctgga cacttggttc agggacaact acgcgctcga acagtgcgtt 360  
 actttctgct aggcgctcat ccagaaggac acctccgacg tgcgctgcac caacggcgaa 420  
 ccgccggttt tcgtcaagcc ggagaaagta gttggagtga ttggggcttc ggggagttcg 480  
 gtctccatca tggtagccaa catcctgagg ctcttcaga tccccagat tagttatgca 540  
 tcaacggcac ccgagctaag tgatgaccgg cgctatgact tcttctctcg cgtggtgccca 600  
 cccgattcct tccaagccca ggccatggta gacattgtaa aggccctagg ctggaattat 660  
 gtgtctaccc tcgcatcgga aggaagttat ggagagaaag gtgtggagtc cttcacgcag 720  
 atttccaaa aggcaggtag actctgcatt gccagtcgc tgagaatccc ccaggaacgc 780  
 aaagacagga ccattgactt tgatagaatt atcaaacagc tcctggacac ccccaactcc 840  
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 agagctgacc aagttggcca ttttctttgg gtgggacag acagctgggg atccaaaata 960  
 aacctactgc accagcatga agatatcgca gaaggggcca tcaccattca gcccaagcga 1020  
 gccacggtg aagggtttga tgcctacttt acgtcccgta cacttgaaaa caacagaaga 1080  
 aatgtatggt ttgccgaata ctgggaggaa aacttcaact gcaagttgac gattagtggg 1140  
 tcaaaaaaag aagacacaga tcgcaaatgc acaggacagg agagaattgg aaaagattcc 1200  
 aactatgagc aggagggtaa agtccagttc gtgattgacg cagtctatgc tatggctcac 1260  
 gcccttcacc acatgaacaa ggatctctgt gctgactacc ggggtgtctg ccagagatg 1320  
 gagcaagctg gaggcaagaa gttgctgaag tatatacgca atgttaattt caatggtagt 1380

gctggcactc cagtgatgtt taacaagaac ggggatgcac ctgggcgtta tgacatcttt 1440  
cagtaccaga ccacaacac cagcaaccgc ggttacgcgc tgatcgggca gtggacagac 1500  
gaacttcagc tcaatataga agacatgcag tggggtaaag gagtcgaga gatacccgcc 1560  
tcagtgtgca cactaccatg taagccagga cagagaaaga agacacagaa aggaactect 1620  
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gagcaagcca gagggttctt caagtgtgac attacagatc tccaaatcat ttgctccttg 2280  
ggatatagca ttcttctcat ggtcacatgt actgtgtatg ccatcaagac tcgggggtgta 2340  
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cgaagcttca aggcggtagt cacagcagcc accatgtcat cgaggctgtc acacaaaccc 2640  
agtgcacagc ccaacgggtg ggcgaagacc gagctctgtg aaaacgtaga cccaaacagc 2700  
cctgctgcaa aaaagaagta tgtcagttat aataacctgg ttatctaa 2748

<210> 73  
<211> 915  
<212> PRT  
<213> Unknown  
  
<220>  
<223> Novel Sequence  
  
<400> 73

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Pro	Cys	Cys	Val	Leu	Glu	Val	Leu	Leu	Cys	Ala	Leu	Ala	Ala	Ala	Ala
			20					25					30		
Arg	Gly	Gln	Glu	Met	Tyr	Ala	Pro	His	Ser	Ile	Arg	Ile	Glu	Gly	Asn
		35					40					45			
Val	Thr	Leu	Gly	Gly	Leu	Phe	Pro	Val	His	Ala	Lys	Gly	Pro	Ser	Gly
	50					55					60				
Val	Pro	Cys	Gly	Asp	Ile	Lys	Arg	Glu	Asn	Gly	Ile	His	Arg	Leu	Glu
65					70					75					80
Ala	Met	Leu	Tyr	Ala	Leu	Asp	Gln	Ile	Asn	Ser	Asp	Pro	Asn	Leu	Leu
				85					90					95	
Pro	Asn	Val	Thr	Leu	Gly	Ala	Arg	Ile	Leu	Asp	Thr	Cys	Ser	Arg	Asp
		100						105					110		
Thr	Tyr	Ala	Leu	Glu	Gln	Ser	Leu	Thr	Phe	Val	Gln	Ala	Leu	Ile	Gln
	115						120					125			
Lys	Asp	Thr	Ser	Asp	Val	Arg	Cys	Thr	Asn	Gly	Glu	Pro	Pro	Val	Phe
130						135					140				
Val	Lys	Pro	Glu	Lys	Val	Val	Gly	Val	Ile	Gly	Ala	Ser	Gly	Ser	Ser
145					150					155					160
Val	Ser	Ile	Met	Val	Ala	Asn	Ile	Leu	Arg	Leu	Phe	Gln	Ile	Pro	Gln
				165					170					175	
Ile	Ser	Tyr	Ala	Ser	Thr	Ala	Pro	Glu	Leu	Ser	Asp	Asp	Arg	Arg	Tyr
			180					185					190		
Asp	Phe	Phe	Ser	Arg	Val	Val	Pro	Pro	Asp	Ser	Phe	Gln	Ala	Gln	Ala
		195					200					205			
Met	Val	Asp	Ile	Val	Lys	Ala	Leu	Gly	Trp	Asn	Tyr	Val	Ser	Thr	Leu
	210					215					220				





450

455

460

Val Met Phe Asn Lys Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe  
465 470 475 480

Gln Tyr Gln Thr Thr Asn Thr Ser Asn Pro Gly Tyr Arg Leu Ile Gly  
485 490 495

Gln Trp Thr Asp Glu Leu Gln Leu Asn Ile Glu Asp Met Gln Trp Gly  
500 505 510

Lys Gly Val Arg Glu Ile Pro Ala Ser Val Cys Thr Leu Pro Cys Lys  
515 520 525

Pro Gly Gln Arg Lys Lys Thr Gln Lys Gly Thr Pro Cys Cys Trp Thr  
530 535 540

Cys Glu Pro Cys Asp Gly Tyr Gln Tyr Gln Phe Asp Glu Met Thr Cys  
545 550 555 560

Gln His Cys Pro Tyr Asp Gln Arg Pro Asn Glu Asn Arg Thr Gly Cys  
565 570 575

Gln Asp Ile Pro Ile Ile Lys Leu Glu Trp His Ser Pro Trp Ala Val  
580 585 590

Ile Pro Val Phe Leu Ala Met Leu Gly Ile Ile Ala Thr Ile Phe Val  
595 600 605

Met Ala Thr Phe Ile Arg Tyr Asn Asp Thr Pro Ile Val Arg Ala Ser  
610 615 620

Gly Arg Glu Leu Ser Tyr Val Leu Leu Thr Gly Ile Phe Leu Cys Tyr  
625 630 635 640

Ile Ile Thr Phe Leu Met Ile Ala Lys Pro Asp Val Ala Val Cys Ser  
645 650 655

Phe Arg Arg Val Phe Leu Gly Leu Gly Met Cys Ile Ser Tyr Ala Ala  
660 665 670

Leu Leu Thr Lys Thr Asn Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys  
675 680 685

Lys Ser Val Thr Ala Pro Arg Leu Ile Ser Pro Thr Ser Gln Leu Ala  
690 695 700

Ile Thr Ser Ser Leu Ile Ser Val Gln Leu Leu Gly Val Phe Ile Trp  
705 710 715 720

Phe Gly Val Asp Pro Pro Asn Ile Ile Ile Asp Tyr Asp Glu His Lys  
725 730 735

Thr Met Asn Pro Glu Gln Ala Arg Gly Val Leu Lys Cys Asp Ile Thr  
740 745 750

Asp Leu Gln Ile Ile Cys Ser Leu Gly Tyr Ser Ile Leu Leu Met Val  
755 760 765

Thr Cys Thr Val Tyr Ala Ile Lys Thr Arg Gly Val Pro Glu Asn Phe  
770 775 780

Asn Glu Ala Lys Pro Lys Gly Phe Thr Met Tyr Thr Thr Cys Ile Val  
785 790 795 800

Trp Leu Ala Phe Ile Pro Ile Phe Phe Gly Thr Ala Gln Ser Ala Glu  
805 810 815

Lys Leu Tyr Ile Gln Thr Thr Thr Leu Thr Ile Ser Met Asn Leu Ser  
820 825 830

Ala Ser Val Ala Leu Gly Met Leu Tyr Met Pro Lys Val Tyr Ile Ile  
835 840 845

Ile Phe His Pro Glu Leu Asn Val Gln Lys Arg Lys Arg Ser Phe Lys  
850 855 860

Ala Val Val Thr Ala Ala Thr Met Ser Ser Arg Leu Ser His Lys Pro  
865 870 875 880

Ser Asp Arg Pro Asn Gly Glu Ala Lys Thr Glu Leu Cys Glu Asn Val  
885 890 895

Asp Pro Asn Ser Pro Ala Ala Lys Lys Lys Tyr Val Ser Tyr Asn Asn  
900 905 910

Leu Val Ile  
915

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<211> 1842  
<212> DNA  
<213> Unknown

<220>  
<223> Novel Sequence

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ggggagagct gtgcacctac agtgatccag cgccgcggca gggacgctg gggaccggga 180  
aattctgcaa gagacgttct gcgagcccg gcacccaggg aggagcaggg ggcagcgttt 240  
cttgccggac cctctggga cctgccggcg gccccgggccc gtgaccggcg tgcaggcaga 300  
ggggcggagg cgtcggcagc cggaccccc ggacctccaa ccaggccacc tggcccctgg 360  
aggtggaagg gtgctcgggg tcaggagcct tctgaaactt tggggagagg gaacccacg 420  
gccctccagc tcttcttca gatctcagag gaggaagaga agggctccag aggcgtggc 480  
atctccgggc gtgaccagga gcagagtgtg aagacagtc ccggagccag cgatctttt 540  
tactggccaa ggagagccgg gaaactccag ggttcccacc acaagcccct gtccaagacg 600  
gccaatggac tggcggggca cgaagggtg acaattgcac tccgggccc ggcgtggcc 660  
cagaatggat ccttgggtga aggaatccat gagcctgggg gtccccccg gggaaacagc 720  
acgaaccggc gtgtgagact gaagaacccc ttctaccgc tgaccagga gtcctatgga 780  
gcctacgcgg tcattgtgtc gtcgtgtgtg atcttcggga ccggcatcat tggcaacctg 840  
gcgggtgatg gcatcgtgtg ccacaactac tacatcgga gcatctccaa ctcccctttg 900  
gccaaacctg ccttctggga ctttctcacc atcttcttct gccttcgct ggtcatcttc 960  
cacgagctga ccaagaagt gctgctggag gacttctcct gcaagatcgt gccctatata 1020  
gaggctgctt ctctgggagt caccaccttc acccgatgtg ctctgtgcat agaccgcttc 1080  
cgtgtgcgca ccaacgtaca gatgtactac gaaatgatcg aaaactgttc ctcaacaact 1140  
gccaaacctg ctgttatatg ggtgggagct ctattgttag cacttcacaga agttgttctc 1200  
cgccagctga gcaaggagga tttggggttt agtggccgag ctccggcaga aaggtgcatt 1260  
attaagatct ctctgatatt accagacacc atctatgttc tagccctcac ctacgacagt 1320

gcgagactgt ggtgggtattt tggctgttac ttttgtttgc ccacgctttt caccatcacc 1380  
 tgctctctag tgactgcgag gaaaatccgc aaagcagaga aagcctgtac ccgaggggaat 1440  
 aaacggcaga ttcaactaga gactcagatg aactgtacag tagtggcact gaccatttta 1500  
 tatggatttt gcattattcc tgaaaatato tgcaacattg ttactgccta catggctaca 1560  
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 atggagtgtc gctgctgttg ctgtgaggaa tgcattcaga agtcttcaac ggtgaccagt 1740  
 gatgacaatg acaacgagta caccacggaa ctggaactct cgcctttcag taccatacgc 1800  
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<210> 75  
 <211> 613  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Novel Sequence

<400> 75

Met Arg Ala Pro Gly Ala Leu Leu Ala Arg Met Ser Arg Leu Leu Leu  
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Leu Leu Leu Leu Lys Val Ser Ala Ser Ser Ala Leu Gly Val Ala Pro  
 20 25 30

Ala Ser Arg Asn Glu Thr Cys Leu Gly Glu Ser Cys Ala Pro Thr Val  
 35 40 45

Ile Gln Arg Arg Gly Arg Asp Ala Trp Gly Pro Gly Asn Ser Ala Arg  
 50 55 60

Asp Val Leu Arg Ala Arg Ala Pro Arg Glu Glu Gln Gly Ala Ala Phe  
 65 70 75 80

Leu Ala Gly Pro Ser Trp Asp Leu Pro Ala Ala Pro Gly Arg Asp Pro  
 85 90 95

Ala Ala Gly Arg Gly Ala Glu Ala Ser Ala Ala Gly Pro Pro Gly Pro  
 100 105 110

Pro Thr Arg Pro Pro Gly Pro Trp Arg Trp Lys Gly Ala Arg Gly Gln  
115 120 125

Glu Pro Ser Glu Thr Leu Gly Arg Gly Asn Pro Thr Ala Leu Gln Leu  
130 135 140

Phe Leu Gln Ile Ser Glu Glu Glu Lys Gly Pro Arg Gly Ala Gly  
145 150 155 160

Ile Ser Gly Arg Ser Gln Glu Gln Ser Val Lys Thr Val Pro Gly Ala  
165 170 175

Ser Asp Leu Phe Tyr Trp Pro Arg Arg Ala Gly Lys Leu Gln Gly Ser  
180 185 190

His His Lys Pro Leu Ser Lys Thr Ala Asn Gly Leu Ala Gly His Glu  
195 200 205

Gly Trp Thr Ile Ala Leu Pro Gly Arg Ala Leu Ala Gln Asn Gly Ser  
210 215 220

Leu Gly Glu Gly Ile His Glu Pro Gly Gly Pro Arg Arg Gly Asn Ser  
225 230 235 240

Thr Asn Arg Arg Val Arg Leu Lys Asn Pro Phe Tyr Pro Leu Thr Gln  
245 250 255

Glu Ser Tyr Gly Ala Tyr Ala Val Met Cys Leu Ser Val Val Ile Phe  
260 265 270

Gly Thr Gly Ile Ile Gly Asn Leu Ala Val Met Cys Ile Val Cys His  
275 280 285

Asn Tyr Tyr Met Arg Ser Ile Ser Asn Ser Leu Leu Ala Asn Leu Ala  
290 295 300

Phe Trp Asp Phe Leu Ile Ile Phe Phe Cys Leu Pro Leu Val Ile Phe  
305 310 315 320

His Glu Leu Thr Lys Lys Trp Leu Leu Glu Asp Phe Ser Cys Lys Ile  
325 330 335



Thr Val Thr Ser Asp Asp Asn Asp Asn Glu Tyr Thr Thr Glu Leu Glu  
580 585 590

Leu Ser Pro Phe Ser Thr Ile Arg Glu Met Ser Thr Phe Ala Ser  
595 600 605

Val Gly Thr His Cys  
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<210> 76  
<211> 1842  
<212> DNA  
<213> Homo sapiens

<400> 76  
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gccaatggac tggcggggca cgaagggtgg acaattgcac tcccggggcg ggcgctggcc 660  
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Leu	Ala	Gly	Pro	Ser	Trp	Asp	Leu	Pro	Ala	Ala	Pro	Gly	Arg	Asp	Pro	
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Ala	Ala	Gly	Arg	Gly	Ala	Glu	Ala	Ser	Ala	Ala	Gly	Pro	Pro	Gly	Pro	
				100					105					110		
Pro	Thr	Arg	Pro	Pro	Gly	Pro	Trp	Arg	Trp	Lys	Gly	Ala	Arg	Gly	Gln	
				115					120					125		
Glu	Pro	Ser	Glu	Thr	Leu	Gly	Arg	Gly	Asn	Pro	Thr	Ala	Leu	Gln	Leu	
				130					135					140		
Phe	Leu	Gln	Ile	Ser	Glu	Glu	Glu	Glu	Lys	Gly	Pro	Arg	Gly	Ala	Gly	
				145					150					155		
Ile	Ser	Gly	Arg	Ser	Gln	Glu	Gln	Ser	Val	Lys	Thr	Val	Pro	Gly	Ala	
				165					170					175		
Ser	Asp	Leu	Phe	Tyr	Trp	Pro	Arg	Arg	Ala	Gly	Lys	Leu	Gln	Gly	Ser	
				180					185					190		
His	His	Lys	Pro	Leu	Ser	Lys	Thr	Ala	Asn	Gly	Leu	Ala	Gly	His	Glu	
				195					200					205		
Gly	Trp	Thr	Ile	Ala	Leu	Pro	Gly	Arg	Ala	Leu	Ala	Gln	Asn	Gly	Ser	
				210					215					220		
Leu	Gly	Glu	Gly	Ile	His	Glu	Pro	Gly	Gly	Pro	Arg	Arg	Gly	Asn	Ser	
				225					230					235		
Thr	Asn	Arg	Arg	Val	Arg	Leu	Lys	Asn	Pro	Phe	Tyr	Pro	Leu	Thr	Gln	
				245					250					255		
Glu	Ser	Tyr	Gly	Ala	Tyr	Ala	Val	Met	Cys	Leu	Ser	Val	Val	Ile	Phe	
				260					265					270		
Gly	Thr	Gly	Ile	Ile	Gly	Asn	Leu	Ala	Val	Met	Cys	Ile	Val	Cys	His	
				275					280					285		
Asn	Tyr	Tyr	Met	Arg	Ser	Ile	Ser	Asn	Ser	Leu	Leu	Ala	Asn	Leu	Ala	
				290					295					300		
Phe	Trp	Asp	Phe	Leu	Ile	Ile	Phe	Phe	Cys	Leu	Pro	Leu	Val	Ile	Phe	



Thr Pro Val Leu Leu Phe Cys Leu Cys Lys Pro Phe Ser Arg Ala Phe  
545 550 555 560

Met Glu Cys Cys Cys Cys Cys Glu Glu Cys Ile Gln Lys Ser Ser  
565 570 575

Thr Val Thr Ser Asp Asp Asn Asp Asn Glu Tyr Thr Thr Glu Leu Glu  
580 585 590

Leu Ser Pro Phe Ser Thr Ile Arg Arg Glu Met Ser Thr Phe Ala Ser  
595 600 605

Val Gly Thr His Cys  
610

<210> 78  
<211> 1086  
<212> DNA  
<213> Unknown

<220>  
<223> Novel Sequence

<400> 78  
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 tacaacatga cactgtgcag gaatgagtgg aagaaaattt ttgtgtgctt ctggttccca 1020  
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 ggctaa 1086

<210> 79  
 <211> 361  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Novel Sequence

<400> 79

Met Ser Pro Glu Cys Ala Arg Ala Ala Gly Asp Ala Pro Leu Arg Ser  
1 5 10 15

Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys  
20 25 30

Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val  
35 40 45

Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu  
50 55 60

Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn  
65 70 75 80

Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu  
85 90 95

Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His  
100 105 110

Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr  
115 120 125

Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln  
130 135 140

Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala  
145 150 155 160

Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe  
165 170 175

Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser  
180 185 190

Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp  
195 200 205

Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val  
210 215 220

Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg  
225 230 235 240

Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser  
245 250 255

Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser  
260 265 270

Phe Phe Ile Met Trp Ser Pro Ile Phe Ile Thr Ile Leu Leu Ile Leu  
275 280 285

Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe  
290 295 300

Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu  
305 310 315 320

Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys  
325 330 335

Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys  
340 345 350

Arg Asn Asp Leu Ser Ile Ile Ser Gly  
355 360

<210> 80  
<211> 1086  
<212> DNA  
<213> Unknown

<220>  
<223> Novel Sequence

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gcggtggaga caacgtgct ggtgctcatc ttgacagtgt cgctgctggg caacgtgtgc 180  
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tcctcttctt tctgggtggt ggccttcaca ttgctaatt cagccctaaa ccccatctc 960  
tacaacatga cactgtgcag gaatgagtgg aagaaaattt ttgctgctt ctggttccca 1020  
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ggctaa 1086

<210> 81  
<211> 361  
<212> PRT  
<213> Unknown

<220>  
<223> Novel Sequence

<400> 81

Met Ser Pro Glu Cys Ala Arg Ala Ala Gly Asp Ala Pro Leu Arg Ser  
1 5 10 15

Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys  
20 25 30

Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val  
35 40 45

Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu  
50 55 60

Val Ala Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn  
65 70 75 80

Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu  
85 90 95

Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His  
100 105 110

Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr  
115 120 125

Leu Ala Ala Val Ser Leu Asn Arg Met Val Cys Ile Val His Leu Gln  
130 135 140

Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala  
145 150 155 160

Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe  
165 170 175

Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser  
180 185 190

Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp  
195 200 205

Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val  
210 215 220





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<210>	83
<211>	403
<212>	PRT
<213>	Unknown

<220>  
<223> Novel Sequence

<400> 83

Met Ala Cys Asn Gly Ser Ala Ala Arg Gly His Phe Asp Pro Glu Asp  
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Leu Asn Leu Thr Asp Glu Ala Leu Arg Leu Lys Tyr Leu Gly Pro Gln  
20 25 30

Gln Thr Glu Leu Phe Met Pro Ile Cys Ala Thr Tyr Leu Leu Ile Phe  
35 40 45

Val Val Gly Ala Val Gly Asn Gly Leu Thr Cys Leu Val Ile Leu Arg  
50 55 60



Pro Phe His Ala Asp Arg Val Met Trp Ser Val Val Ser Gln Trp Thr  
290 295 300

Asp Gly Leu His Leu Ala Phe Gln His Val His Val Ile Ser Gly Ile  
305 310 315 320

Phe Phe Tyr Leu Gly Ser Ala Ala Asn Pro Val Leu Tyr Ser Leu Met  
325 330 335

Ser Ser Arg Phe Arg Glu Thr Phe Gln Glu Ala Leu Cys Leu Gly Ala  
340 345 350

Cys Cys His Arg Leu Arg Pro Arg His Ser Ser His Ser Leu Ser Arg  
355 360 365

Met Thr Thr Gly Ser Thr Leu Cys Asp Val Gly Ser Leu Gly Ser Trp  
370 375 380

Val His Pro Leu Ala Gly Asn Asp Gly Pro Glu Ala Gln Gln Glu Thr  
385 390 395 400

Asp Pro Ser

<210> 84  
<211> 930  
<212> DNA  
<213> Unknown

<220>  
<223> Novel Sequence

<400> 84  
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gcgcctctggg tgttctgctg ccgcatgcag cagtggacgg agaccgcgat ctacatgacc 180  
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tacctagagca tcagcctggt caccggccatc gccgtggacc gctatgtggc cgtgcggcac 360  
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<210> 85
<211> 309
<212> PRT
<213> Unknown

<220>
<223> Novel Sequence

<400> 85

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Met Asn Gly Thr Tyr Asn Thr Cys Gly Ser Ser Asp Leu Thr Trp Pro
1          5          10          15

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```

Pro Ala Ile Lys Leu Gly Phe Tyr Ala Tyr Leu Gly Val Leu Leu Val
          20          25          30

```

```

Leu Gly Leu Leu Leu Asn Ser Leu Ala Leu Trp Val Phe Cys Cys Arg
          35          40          45

```

```

Met Gln Gln Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val
          50          55          60

```

```

Ala Asp Leu Cys Leu Leu Cys Thr Leu Pro Phe Val Leu His Ser Leu
          65          70          75          80

```

```

Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu Ser Gln Gly Ile Tyr
          85          90          95

```

```

Leu Thr Asn Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val
          100          105          110

```

```

Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Gly Leu Arg
          115          120          125

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<400> 86
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tgctga 1446
  
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<210> 87
<211> 481
<212> PRT
<213> Unknown
  
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<220>

<223> Novel Sequence

<400> 87

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Val Gly Leu Ser Arg Val Ser Gly Gly Ala Pro Leu His Leu Gly Arg  
20 25 30

His Arg Ala Glu Thr Gln Glu Gln Gln Ser Arg Ser Lys Arg Gly Thr  
35 40 45

Glu Asp Glu Glu Ala Lys Gly Val Gln Gln Tyr Val Pro Glu Glu Trp  
50 55 60

Ala Glu Tyr Pro Arg Pro Ile His Pro Ala Gly Leu Gln Pro Thr Lys  
65 70 75 80

Pro Leu Val Ala Thr Ser Pro Asn Pro Asp Lys Asp Gly Gly Thr Pro  
85 90 95

Asp Ser Gly Gln Glu Leu Arg Gly Asn Leu Thr Gly Ala Pro Gly Gln  
100 105 110

Arg Leu Gln Ile Gln Asn Pro Leu Tyr Pro Val Thr Glu Ser Ser Tyr  
115 120 125

Ser Ala Tyr Ala Ile Met Leu Leu Ala Leu Val Val Phe Ala Val Gly  
130 135 140

Ile Val Gly Asn Leu Ser Val Met Cys Ile Val Trp His Ser Tyr Tyr  
145 150 155 160

Leu Lys Ser Ala Trp Asn Ser Ile Leu Ala Ser Leu Ala Leu Trp Asp  
165 170 175

Phe Leu Val Leu Phe Phe Cys Leu Pro Ile Val Ile Phe Asn Glu Ile  
180 185 190

Thr Lys Gln Arg Leu Leu Gly Asp Val Ser Cys Arg Ala Val Pro Phe  
195 200 205





Cys Cys Cys Cys Glu Glu Cys Gly Gly Ala Ser Glu Ala Ser Ala Ala  
 435 440 445

Asn Gly Ser Asp Asn Lys Leu Lys Thr Glu Val Ser Ser Ser Ile Tyr  
 450 455 460

Phe His Lys Pro Arg Glu Ser Pro Pro Leu Leu Pro Leu Gly Thr Pro  
 465 470 475 480

Cys

<210> 88  
 <211> 6  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Novel Sequence

<400> 88

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 1 5

<210> 89  
 <211> 5  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Novel Sequence

<400> 89

Glu Tyr Asn Leu Val  
 1 5

<210> 90  
 <211> 5  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Novel Sequence

<400> 90

Asp Cys Gly Leu Phe  
 1 5

<210> 91  
 <211> 34  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Novel Sequence

<400> 91  
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34

<210> 92  
 <211> 53  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Novel Sequence

<400> 92  
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53

<210> 93  
 <211> 5  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Novel Sequence

<400> 93  
 Gln Tyr Glu Leu Leu  
 1 5

<210> 94  
 <211> 5  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Novel Sequence

<400> 94  
 Asp Cys Gly Leu Phe  
 1 5

<210> 95  
 <211> 1185  
 <212> DNA  
 <213> Unknown

<220>

<223> Novel Sequence

<400> 95

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<212> PRT

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Asp Lys Gln Val Tyr Arg Ala Thr His Arg Leu Leu Leu Gly Ala  
35 40 45

Gly Glu Ser Gly Lys Ser Thr Ile Val Lys Gln Met Arg Ile Leu His  
50 55 60

Val Asn Gly Phe Asn Gly Glu Gly Gly Glu Glu Asp Pro Gln Ala Ala  
65 70 75 80

Arg Ser Asn Ser Asp Gly Glu Lys Ala Thr Lys Val Gln Asp Ile Lys  
85 90 95

Asn Asn Leu Lys Glu Ala Ile Glu Thr Ile Val Ala Ala Ser Asn Leu  
100 105 110

Val Pro Pro Val Glu Leu Ala Asn Pro Glu Asn Gln Phe Arg Val Asp  
115 120 125

Tyr Ile Leu Ser Val Met Asn Val Pro Asn Phe Asp Phe Pro Pro Glu  
130 135 140

Phe Tyr Glu His Ala Lys Ala Leu Trp Glu Asp Glu Gly Val Arg Ala  
145 150 155 160

Cys Tyr Glu Arg Ser Asn Glu Tyr Gln Leu Ile Asp Cys Ala Gln Tyr  
165 170 175

Phe Leu Asp Lys Ile Asp Val Ile Lys Gln Ala Asp Tyr Val Pro Ser  
180 185 190

Asp Gln Asp Leu Leu Arg Cys Arg Val Leu Thr Ser Gly Ile Phe Glu  
195 200 205

Thr Lys Phe Gln Val Asp Lys Val Asn Phe His Met Phe Asp Val Gly  
210 215 220

Gly Gln Arg Asp Glu Arg Arg Lys Trp Ile Gln Cys Phe Asn Asp Val  
225 230 235 240



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<210> 98  
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 <212> PRT  
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<400> 98

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Ser Ala Asp Ile Arg Arg Gln Ala Pro Ala Leu Phe Thr Leu Asn Leu  
 35 40 45

Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu  
 50 55 60

Ala Gly Val Val Ala Gln Arg Gln Pro Ala Gly Asp Arg Leu Cys Arg  
 65 70 75 80

Leu Ala Ala Phe Leu Asp Thr Phe Leu Ala Ala Asn Ser Met Leu Ser  
 85 90 95

Met Ala Ala Leu Ser Ile Asp Arg Trp Val Ala Val Val Phe Pro Leu  
100 105 110

Ser Tyr Arg Ala Lys Met Pro Pro Pro Arg Cys Ala Leu Ile Leu Ala  
115 120 125

Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Ala Ala Leu Ala Leu  
130 135 140

Ser Trp Leu Gly Phe His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser  
145 150 155 160

Arg Arg Pro Asp Glu Arg Leu Arg Phe Ala Val Phe Thr Gly Ala Phe  
165 170 175

His Ala Leu Ser Phe Leu Leu Ser Phe Val Val Leu Cys Cys Thr Tyr  
180 185 190

Leu Lys Val Leu Lys Val Ala Arg Phe His Cys Lys Arg Ile Asp Val  
195 200 205

Ile Thr Met Gln Thr Leu Val Leu Leu Val Asp Leu His Pro Ser Val  
210 215 220

Arg Glu Arg Cys Leu Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr  
225 230 235 240

Lys Lys Ile Ser Thr Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro  
245 250 255

Tyr Val Ile Thr Arg Leu Val Glu Leu Phe Ser Thr Val Pro Ile Gly  
260 265 270

Ser His Trp Gly Val Leu Ser Lys Cys Leu Ala Tyr Ser Lys Ala Ala  
275 280 285

Ser Asp Pro Phe Val Tyr Ser Leu Leu Arg His Gln Tyr Arg Lys Ser  
290 295 300

Cys Lys Glu Ile Leu Asn Arg Leu Leu His Arg Arg Ser Ile His Ser  
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Ser Gly Leu Thr Gly Asp Ser His Ser Gln Asn Ile Leu Pro Val Ser



Glu

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 <211> 21  
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<220>  
 <223> Novel Sequence

<400> 99  
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 <211> 30  
 <212> DNA  
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<220>  
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<400> 100  
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<210> 101  
 <211> 36  
 <212> DNA  
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<220>  
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<400> 101  
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<210> 102  
 <211> 32  
 <212> DNA  
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<220>  
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<400> 102  
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32